

Package: fluentGenomics (via r-universe)

October 4, 2026

Type Package

Title A plyranges and tximeta workflow

Version 1.24.0

Description An extended workflow using the plyranges and tximeta packages for fluent genomic data analysis. Use tximeta to correctly import RNA-seq transcript quantifications and summarize them to gene counts for downstream analysis. Use plyranges for clearly expressing operations over genomic coordinates and to combine results from differential expression and differential accessibility analyses.

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Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.0.2

VignetteBuilder knitr, rmarkdown

Depends R (>= 4.0)

Imports plyranges (>= 1.7.7), dplyr, SummarizedExperiment, readr, stats, utils

Suggests knitr, rmarkdown, bookdown, rappdirs, BiocFileCache, DESeq2, limma, ggplot2, tidyr, tximeta (>= 1.4.2), macrophage (>= 1.2.0),

biocViews Workflow, BasicWorkflow, GeneExpressionWorkflow

Workflow true

URL <https://github.com/sa-lee/fluentGenomics>

BugReports <https://github.com/sa-lee/fluentGenomics/issues>

Config/pak/sysreqs

make libbz2-dev liblzma-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

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RemoteUrl `https://github.com/bioc/fluentGenomics`
RemoteRef `RELEASE_3_23`
RemoteSha `ab4340df7cba28a1066f36d935ff28204b4fe249`

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cache_atac_se	<i>Download, retrieve and cache macrophage ATAC seq results</i>
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Description

Download, retrieve and cache macrophage ATAC seq results

Usage

`cache_atac_se(verbose = FALSE)`

Arguments

<code>verbose</code>	Provide progress bar for downloading and updating the cache? (Default is FALSE)
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Details

This code generates the SummarizedExperiment object used for ATAC seq peaks data analysis as discussed in the vignette.

Value

the path to the .rds file containing the SummarizedExperiment

Source

<https://zenodo.org/record/1188300/files/>

Examples

```
if (interactive()) {  
  path_to_se <- cache_atac_se()  
  atac <- readRDS(path_to_se)  
}
```

peaks*Summarised ATAC-seq peaks as a GRanges object*

Description

A GRanges object containing approximately 300,000 differential accessibility peaks estimated via limma. A description of how this object was generated can be found in the vignette.

Usage

peaks

Format

An object of class GRanges of length 296220.

Details

#' @format A GRanges with 296220 rows and 3 metadata columns:

peak_id the ATAC peak identifier

da_log2FC the estimated log2 fold change

da_padj the estimated differential accessibility FDR adjusted p-value

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* **datasets**

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